

DSO
1119

Page 1 of 7

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P.5

75

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/825,561A

DATE: 10/17/2001
TIME: 12:23:45

Input Set : A:\00-22SEQ.txt
Output Set: N:\CRF3\10172001\I825561A.raw

4 <110> APPLICANT: Sprecher, Cindy A.
5 Novak, Julia E.
6 West, James W.
7 Presnell, Scott R.
8 Holly, Richard D.
9 Nelson, Andrew J.
12 <120> TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
15 <130> FILE REFERENCE: 00-22
C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/825,561A
C--> 17 <141> CURRENT FILING DATE: 2000-04-05
17 <150> PRIOR APPLICATION NUMBER: US 60/194,731
18 <151> PRIOR FILING DATE: 2000-04-05
20 <150> PRIOR APPLICATION NUMBER: US 60/222,121
21 <151> PRIOR FILING DATE: 2000-07-28
23 <160> NUMBER OF SEQ ID NOS: 86
25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1614
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)...(1614)
36 <400> SEQUENCE: 1
37 atg ccg cgt ggc tgg gcc ccc ttg ctc ctg ctg ctc cag gga 48
38 Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly
39 1 5 10 15
41 ggc tgg ggc tgc ccc gac ctc gtc tac acc gat tac ctc cag acg 96
42 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
43 20 25 30
45 gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc 144
46 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
47 35 40 45
49 ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc 192
50 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
51 50 55 60
53 tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc 240
54 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
55 65 70 75 80
57 tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc 288
58 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
59 85 90 95
61 aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt 336
62 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
63 100 105 110
65 ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg 384
66 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val

ENTERED

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Input Set : A:\00-22SEQ.txt
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67	115	120	125	
69	acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac			432
70	Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp			
71	130	135	140	
73	cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac			480
74	Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr			
75	145	150	155	160
77	agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc			528
78	Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile			
79	165	170	175	
81	tca gtg gac tca aga agt gtc tcc ctc ccc ctg gag ttc cgc aaa			576
82	Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys			
83	180	185	190	
87	gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc			624
88	Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser			
89	195	200	205	
91	tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag			672
92	Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln			
93	210	215	220	
95	acc cag tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt			720
96	Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu			
97	225	230	235	240
99	ctc ctc ctg ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag			768
100	Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys			
101	245	250	255	
103	acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc			816
104	Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser			
105	260	265	270	
107	cct gag cgg ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc			864
108	Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe			
109	275	280	285	
111	aag aaa tgg gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga			912
112	Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly			
113	290	295	300	
115	ccc tgg agc cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac			960
116	Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His			
117	305	310	315	320
119	cca cca cgg agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa			1008
120	Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu			
121	325	330	335	
123	cca gca gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg			1056
124	Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp			
125	340	345	350	
127	ccg aca gcc cag aac tcc ggg ggc tca gct tac agt gag gag agg gat			1104
128	Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp			
129	355	360	365	
131	cgg cca tac ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca			1152
132	Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala			
133	370	375	380	

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135	gag	ggg	cca	tgc	acc	tgg	ccc	tgc	agc	tgt	gag	gat	gac	ggc	tac	cca	1200
136	Glu	Gly	Pro	Cys	Thr	Trp	Pro	Cys	Ser	Cys	Glu	Asp	Asp	Gly	Tyr	Pro	
137	385				390				395							400	
139	gcc	ctg	gac	ctg	gat	gct	ggc	ctg	gag	ccc	agc	cca	ggc	cta	gag	gac	1248
140	Ala	Leu	Asp	Leu	Asp	Ala	Gly	Leu	Glu	Pro	Ser	Pro	Gly	Leu	Glu	Asp	
141					405				410							415	
143	cca	ctc	ttg	gat	gca	ggg	acc	aca	gtc	ctg	tcc	tgt	ggc	tgt	gtc	tca	1296
144	Pro	Leu	Leu	Asp	Ala	Gly	Thr	Thr	Val	Leu	Ser	Cys	Gly	Cys	Val	Ser	
145					420				425							430	
147	gct	ggc	agc	cct	ggg	cta	gga	ggg	ccc	ctg	gga	agc	ctc	ctg	gac	aga	1344
148	Ala	Gly	Ser	Pro	Gly	Leu	Gly	Gly	Pro	Leu	Gly	Ser	Leu	Leu	Asp	Arg	
149					435				440							445	
151	cta	aag	cca	ccc	ctt	gca	gat	ggg	gag	gac	tgg	gct	ggg	gga	ctg	ccc	1392
152	Leu	Lys	Pro	Pro	Leu	Ala	Asp	Gly	Glu	Asp	Trp	Ala	Gly	Gly	Leu	Pro	
153					450				455							460	
155	tgg	ggc	cgg	tca	cct	gga	ggg	gtc	tca	gag	agt	gag	gag	gct	ggc	tca	1440
156	Trp	Gly	Gly	Arg	Ser	Pro	Gly	Gly	Val	Ser	Glu	Ser	Glu	Ala	Gly	Ser	
157					465				470							480	
159	ccc	ctg	gcc	ggc	ctg	gat	atg	gac	acg	ttt	gac	agt	ggc	ttt	gtg	ggc	1488
160	Pro	Leu	Ala	Gly	Leu	Asp	Met	Asp	Thr	Phe	Asp	Ser	Gly	Phe	Val	Gly	
161					485				490							495	
163	tct	gac	tgc	agc	agc	cct	gtg	gag	tgt	gac	ttc	acc	agc	ccc	ggg	gac	1536
164	Ser	Asp	Cys	Ser	Ser	Pro	Val	Glu	Cys	Asp	Phe	Thr	Ser	Pro	Gly	Asp	
165					500				505							510	
167	gaa	gga	ccc	ccc	cgg	agc	tac	ctc	cgc	cag	tgg	gtg	gtc	att	cct	ccg	1584
168	Glu	Gly	Pro	Pro	Arg	Ser	Tyr	Leu	Arg	Gln	Trp	Val	Val	Val	Ile	Pro	Pro
169					515				520							525	
173	cca	ctt	tgc	agc	cct	gga	ccc	cag	gcc	agc							1614
174	Pro	Leu	Ser	Ser	Pro	Gly	Pro	Gln	Ala	Ser							
175					530				535								
178	<210> SEQ ID NO: 2																
179	<211> LENGTH: 538																
180	<212> TYPE: PRT																
181	<213> ORGANISM: Homo sapiens																
183	<400> SEQUENCE: 2																
184	Met	Pro	Arg	Gly	Trp	Ala	Ala	Pro	Leu	Leu	Leu	Leu	Leu	Gln	Gly		
185	1				5				10						15		
186	Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	Thr	
187					20				25						30		
188	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr	
189					35				40						45		
190	Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	
191					50				55						60		
192	Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	
193					65				70						75		80
194	Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	
195					85				90						95		
196	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe	
197					100				105						110		

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/825,561A

DATE: 10/17/2001

TIME: 12:23:45

Input Set : A:\00-22SEQ.txt

Output Set: N:\CRF3\10172001\I825561A.raw

198 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
 199 115 120 125
 200 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 201 130 135 140
 202 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 203 145 150 155 160
 204 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 205 165 170 175
 206 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 207 180 185 190
 208 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 209 195 200 205
 210 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 211 210 215 220
 212 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu
 213 225 230 235 240
 214 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
 215 245 250 255
 216 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
 217 260 265 270
 218 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
 219 275 280 285
 220 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
 221 290 295 300
 222 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
 223 305 310 315 320
 224 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
 225 325 330 335
 226 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
 227 340 345 350
 228 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
 229 355 360 365
 230 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
 231 370 375 380
 232 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
 233 385 390 395 400
 234 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
 235 405 410 415
 236 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Val Ser
 237 420 425 430
 238 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
 239 435 440 445
 240 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
 241 450 455 460
 242 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
 243 465 470 475 480
 244 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
 245 485 490 495
 246 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp

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DATE: 10/17/2001

PATENT APPLICATION: US/09/825,561A

TIME: 12:23:45

Input Set : A:\00-22SEQ.txt

Output Set: N:\CRF3\10172001\I825561A.raw

247	500	505	510														
248	Glu	Gly	Pro	Pro	Arg	Ser	Tyr	Leu	Arg	Gln	Trp	Val	Val	Ile	Pro	Pro	
249			515					520						525			
250	Pro	Leu	Ser	Ser	Pro	Gly	Pro	Gln	Ala	Ser							
251					530			535									
253	<210>	SEQ	ID	NO:	3												
254	<211>	LENGTH:	696														
255	<212>	TYPE:	DNA														
256	<213>	ORGANISM:	Homo sapiens														
259	<220>	FEATURE:															
260	<221>	NAME/KEY:	CDS														
261	<222>	LOCATION:	(1)...(696)														
263	<400>	SEQUENCE:	3														
264	ctg	aac	acg	aca	att	ctg	acg	ccc	aat	ggg	aat	gaa	gac	acc	aca	gct	48
265	Leu	Asn	Thr	Thr	Ile	Leu	Thr	Pro	Asn	Gly	Asn	Glu	Asp	Thr	Thr	Ala	
266	1				5				10			15					
268	gat	tcc	tcc	ctg	acc	act	atg	ccc	act	gac	tcc	ctc	agt	gtt	tcc	act	96
269	Asp	Phe	Phe	Leu	Thr	Thr	Met	Pro	Thr	Asp	Ser	Leu	Ser	Val	Ser	Thr	
270					20				25			30					
272	ctg	ccc	ctc	cca	gag	gtt	cag	tgt	ttt	gtg	ttc	aat	gtc	gag	tac	atg	144
273	Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val	Phe	Asn	Val	Glu	Tyr	Met	
274					35				40			45					
276	aat	tgc	act	tgg	aac	agc	agc	tct	gag	ccc	cag	cct	acc	aac	ctc	act	192
277	Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro	Gln	Pro	Thr	Asn	Leu	Thr	
278					50				55			60					
280	ctg	cat	tat	tgg	tac	aag	aac	tcg	gat	aat	gat	aaa	gtc	cag	aag	tgc	240
281	Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn	Asp	Lys	Val	Gln	Lys	Cys	
282					65				70			75			80		
284	agc	cac	tat	cta	ttc	tct	gaa	gaa	atc	act	tct	ggc	tgt	cag	ttg	caa	288
285	Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr	Ser	Gly	Cys	Gln	Leu	Gln	
286					85				90			95					
288	aaa	aag	gag	atc	cac	ctc	tac	caa	aca	ttt	gtt	gtt	cag	ctc	cag	gac	336
289	Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe	Val	Val	Gln	Leu	Gln	Asp	
290					100				105			110					
292	cca	cgg	gaa	ccc	agg	aga	cag	gcc	aca	cag	atg	cta	aaa	ctg	cag	aat	384
293	Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln	Met	Leu	Lys	Leu	Gln	Asn	
294					115				120			125					
296	ctg	gtg	atc	ccc	tgg	gct	cca	gag	aac	cta	aca	ctt	cac	aaa	ctg	agt	432
297	Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu	Thr	Leu	His	Lys	Leu	Ser	
298					130				135			140					
302	gaa	tcc	cag	cta	gaa	ctg	aac	tgg	aac	aaa	gag	ttc	ttg	aac	cac	tgt	480
303	Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn	Arg	Phe	Leu	Asn	His	Cys	
304					145				150			155			160		
306	ttg	gag	cac	ttg	gtg	cag	tac	cg	act	gac	tgg	gac	cac	agc	tgg	act	528
307	Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp	Trp	Asp	His	Ser	Trp	Thr	
308					165				170			175					
310	gaa	caa	tca	gtg	gat	tat	aga	cat	aag	ttc	tcc	ttg	cct	agt	gtg	gat	576
311	Glu	Gln	Ser	Val	Asp	Tyr	Arg	His	Lys	Phe	Ser	Leu	Pro	Ser	Val	Asp	
312					180				185			190					

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 10/17/2001
PATENT APPLICATION: US/09/825,561A TIME: 12:23:46

Input Set : A:\00-22SEQ.txt
Output Set: N:\CRF3\10172001\I825561A.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:2392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
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L:2398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:2419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:2578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71
L:2581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71